

1600

## RAW SEQUENCE LISTING

DATE: 10/25/2001

PATENT APPLICATION: US/09/582,328

TIME: 13:23:48

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3 <110> APPLICANT: FORSSMANN, WOLF-GEORG  
 4 MAGERT, HANS-JURGEN  
 5 STANDKER, LUDGER  
 6 KREUZTMANN, PETER  
 8 <120> TITLE OF INVENTION: SERINE PROTEINASE INHIBITORS  
 10 <130> FILE REFERENCE: 10496/P65678US0  
 12 <140> CURRENT APPLICATION NUMBER: 09/582,328  
 C--> 13 <141> CURRENT FILING DATE: 2000-07-09  
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/08424  
 16 <151> PRIOR FILING DATE: 1998-12-23  
 18 <150> PRIOR APPLICATION NUMBER: DE 197 57 572.2  
 19 <151> PRIOR FILING DATE: 1997-12-23  
 21 <160> NUMBER OF SEQ ID NOS: 41  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 177  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Unknown Organism  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Description of Unknown Organism: VAKTI-1 amino  
 32 acid sequence  
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 35 Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu  
 36 1 5 10 15  
 38 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu  
 39 20 25 30  
 41 Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys  
 42 35 40 45  
 44 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala  
 45 50 55 60  
 47 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala  
 48 65 70 75 80  
 50 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn  
 51 85 90 95  
 53 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro  
 54 100 105 110  
 56 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn  
 57 115 120 125  
 59 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly  
 60 130 135 140  
 62 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg  
 63 145 150 155 160  
 65 Ser Ile Val Ser Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser  
 66 165 170 175  
 68 Lys  
 71 <210> SEQ ID NO: 2  
 72 <211> LENGTH: 922

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73 &lt;212&gt; TYPE: PRT

74 &lt;213&gt; ORGANISM: Unknown Organism

76 &lt;220&gt; FEATURE:

77 <223> OTHER INFORMATION: Description of Unknown Organism: VATKI-2 amino  
78 acid sequence

80 &lt;400&gt; SEQUENCE: 2

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81 Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
82   1           5           10           15
84 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
85           20           25           30
87 Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
88           35           40           45
90 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
91           50           55           60
93 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
94   65           70           75           80
96 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
97           85           90           95
99 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
100           100           105           110
102 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
103           115           120           125
105 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
106           130           135           140
108 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
109 145           150           155           160
111 Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr
112           165           170           175
114 Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
115           180           185           190
117 Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
118           195           200           205
120 Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
121           210           215           220
123 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
124 225           230           235           240
126 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
127           245           250           255
129 Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
130           260           265           270
132 Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
133           275           280           285
135 Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
136           290           295           300
138 Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
139 305           310           315           320
141 Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
142           325           330           335
144 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg

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145          340          345          350
147 Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
148          355          360          365
150 Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
151          370          375          380
153 Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
154 385          390          395          400
156 Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys
157          405          410          415
159 Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
160          420          425          430
162 Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
163          435          440          445
165 Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
166          450          455          460
168 Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
169 465          470          475          480
171 Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
172          485          490          495
174 Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
175          500          505          510
177 Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
178          515          520          525
180 Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
181          530          535          540
183 Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
184 545          550          555          560
186 Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
187          565          570          575
189 Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
190          580          585          590
192 Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
193          595          600          605
195 Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
196          610          615          620
198 Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
199 625          630          635          640
201 Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
202          645          650          655
204 Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe
205          660          665          670
207 Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg
208          675          680          685
210 Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Gly Asn Thr Gln
211          690          695          700
213 Asp Glu Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser
214 705          710          715          720
216 Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr
217          725          730          735

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219 Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu
220           740           745           750
222 Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu
223           755           760           765
225 Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly
226           770           775           780
228 Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly
229 785           790           795           800
231 Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg
232           805           810           815
234 Glu Ala Ala Glu Lys Lys Arg Lys Arg Met Lys Thr Gly Ala Ile Gln
235           820           825           830
237 Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys
238           835           840           845
240 Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro
241           850           855           860
243 Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile
244 865           870           875           880
246 Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu
247           885           890           895
249 Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln
250           900           905           910
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253           915           920
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 55
258 <212> TYPE: PRT
259 <213> ORGANISM: Unknown Organism
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Unknown Organism: HF 6479 amino
263     acid sequence
265 <400> SEQUENCE: 3
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267   1           5           10           15
269 Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln Ser Leu
270           20           25           30
272 Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met Ile Leu
273           35           40           45
275 Glu Lys Glu Ala Lys Ser Gln
276           50           55
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280 <211> LENGTH: 68
281 <212> TYPE: PRT
282 <213> ORGANISM: Unknown Organism
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Unknown Organism: HF 7665 amino
286     acid sequence
288 <400> SEQUENCE: 4
289 Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg

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290      1              5              10              15
292 Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro
293              20              25              30
295 Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys
296              35              40              45
298 Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys Lys Glu Gly
299              50              55              60
301 Glu Ser Arg Asn
302 65
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 748
307 <212> TYPE: DNA
308 <213> ORGANISM: Unknown Organism
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Unknown Organism: VAKTI-1 cDNA
312     sequence
314 <220> FEATURE:
315 <221> NAME/KEY: CDS
316 <222> LOCATION: (43)..(573)
318 <400> SEQUENCE: 5
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320                               Met Lys Ile Ala
321                               1
323 aca gtg tca gtg ctt ctg ccc ttg gct ctt tgc ctc ata caa gat gct      102
324 Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala
325 5              10              15              20
327 gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt      150
328 Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe
329              25              30              35
331 atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa      198
332 Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln
333              40              45              50
335 agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg      246
336 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met
337              55              60              65
339 ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca      294
340 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala
341              70              75              80
343 aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt      342
344 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe
345 85              90              95              100
347 aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa      390
348 Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu
349              105              110              115
351 gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg      438
352 Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu
353              120              125              130
355 tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa      486
356 Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu

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**VERIFICATION SUMMARY**

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